09866020Results

SEQ ID NO: 1

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	516	19.2	2273	4	US-09-177-650-88	Sequence 88, Appl
2	510	18.9	2169	4	US-09-105-058C-22	Sequence 22, Appl
3	465.4	17.3	896	4	US-09-105-058C-1	Sequence 1, Appli
4	464	17.2	2814	4	US-09-177-650-90	Sequence 90, Appl
5	460.8	17.1	2565	4	US-09-105-058C-26	Sequence 26, Appl
6	460.8	17.1	2914	4	US-09-177-650-6	Sequence 6, Appli
7	425	15.8	3287	4	US-09-105-058C-19	Sequence 19, Appl
8	423.4	15.7	3232	4	US-09-177-650-1	Sequence 1, Appli
9	423.4	15.7	3237	4	US-09-177-650-95	Sequence 95, Appl
10	421.4	15.6	900	4	US-09-105-058C-3	Sequence 3, Appli
11	420.6	15.6	900	4	US-09-105-058C-5	Sequence 5, Appli
12	363.8	13.5	930	4	US-09-105-058C-17	Sequence 17, Appl
13	334.2	12.4	735	4	US-09-105-058C-7	Sequence 7, Appli
14	267.8	9.9	2028	4	US-09-634-920-1	Sequence 1, Appli
15	267.8	9.9	3181	3	US-09-135-021-1	Sequence 1, Appli
16	267.8	9.9	3181	4	US-09-135-020-1	Sequence 1, Appli

RESULT 1
PCT-US01-09328-2
; Sequence 2, Application PC/TUS0109328
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: KCNQ5, a Novel Potassium Channel
; FILE REFERENCE: 018512-005010PC
; CURRENT APPLICATION NUMBER: PCT/US01/09328
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCNQ5-1
PCT-US01-09328-2

Query Match 100.0%; Score 2694; DB 1; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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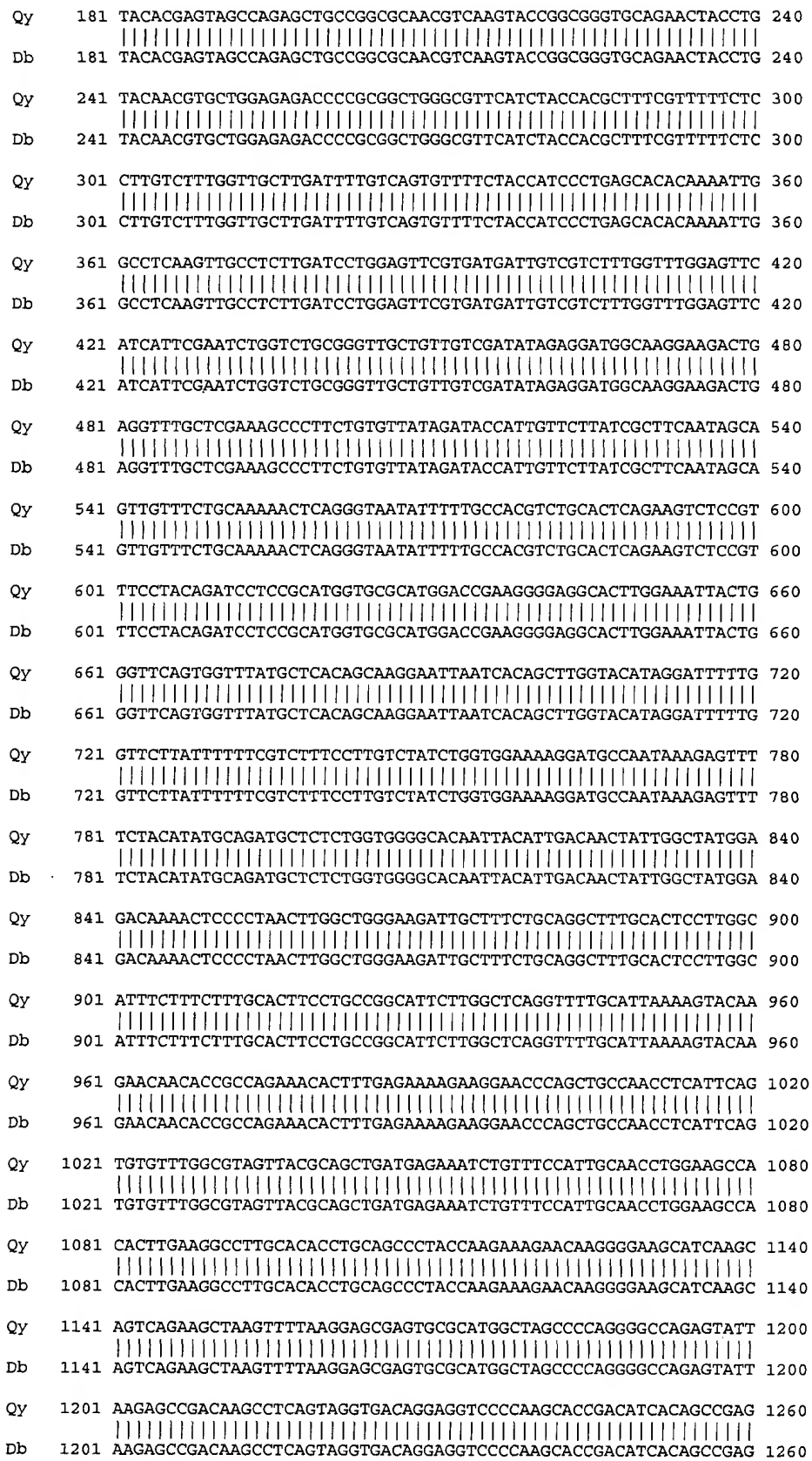
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SUMMARIES

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DEFINITION  Sequence 1 from Patent WO0192526.
ACCESSION   AX322509
VERSION     AX322509.1  GI:18093555
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dworetzky,S.I., Ramanathan,C.S., Trojnacki,J.T., Boissard,C.G. and
            Gribkoff,V.K.
  TITLE     Human kcnq5 potassium channel, methods and compositions thereof
  JOURNAL   Patent: WO 0192526-A 1 06-DEC-2001;
            Bristol-Myers Squibb Company (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 2694;  DB 6;  Length 2694;
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  Matches 2694;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
AF202977
LOCUS       AF202977               3137 bp    mRNA    linear   PRI 01-AUG-2000
DEFINITION  Homo sapiens potassium voltage-gated channel, KQT-like subfamily,
            member 5 (KCNQ5) mRNA, complete cds.
ACCESSION   AF202977
VERSION     AF202977.1  GI:7798695
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3137)
  AUTHORS   Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
            Jentsch,T.J.
  TITLE     KCNQ5, a novel potassium channel broadly expressed in brain,
            mediates M-type currents
  JOURNAL   J. Biol. Chem. 275 (31), 24089-24095 (2000)
  MEDLINE   20379054
   PUBMED   10816588
REFERENCE   2  (bases 1 to 3137)
  AUTHORS   Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
            Jentsch,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistrasse
            85, Hamburg 20246, Germany
FEATURES             Location/Qualifiers
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BASE COUNT 865 a 749 c 745 g 778 t
ORIGIN

Query Match 99.8%; Score 2689.2; DB 9; Length 3137;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy    301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Qy    361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Qy    421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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  AUTHORS   Lerche,C., Scherer,C.R., Seebohm,G., Derst,C., Wei,A.D., Busch,A.E.
            and Steinmeyer,K.
  TITLE     Molecular cloning and functional expression of KCNQ5, a potassium
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channel subunit that may contribute to neuronal M-current diversity
JOURNAL J. Biol. Chem. 275 (29), 22395-22400 (2000)
MEDLINE 20357367
PUBMED 10787416
REFERENCE 2 (bases 1 to 3074)
AUTHORS Lerche,C., Scherer,C.R., Seebohm,G., Derst,C., Wei,A.D., Busch,A.E. and Steinmeyer,K.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2000) Cardiovascular Diseases, Aventis Pharma Deutschland GmbH, Building H824, Frankfurt a. M. 65926, Germany

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ORIGIN

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Db   1835 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1894

Qy   1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
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Qy   1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
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Qy   1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
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Qy   1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
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Qy   1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
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Qy   2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
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Db   2375 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2434

Qy   2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
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Qy   2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
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Qy   2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
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Db   2615 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2674

Qy   2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
```

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Qy   2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
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Db   2735 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2794

Qy   2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
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Qy   2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 15
AB000497
LOCUS       AB000497               2827 bp    mRNA    linear   ROD 23-JAN-1999
DEFINITION  Mus musculus mRNA for alternative splicing:see accession between
            AB000494 and AB000504, complete cds.
ACCESSION   AB000497
VERSION     AB000497.1  GI:4176399
KEYWORDS    mKQT2.4; alternative splicing.
SOURCE      Mus musculus cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T.,
            Sasai,H. and Nishi,Y.
  TITLE     KQT2, a new putative potassium channel family produced by
            alternative splicing. Isolation, genomic structure, and alternative
            splicing of the putative potassium channels
  JOURNAL   Recept. Channels 5 (5), 255-271 (1998)
  MEDLINE   98330948
REFERENCE   2  (bases 1 to 2827)
  AUTHORS   Watanabe,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-1997) Hirotaka Watanabe, Japan Tobacco, Inc.,
            Pharmaceutical Basic Research Lab.; 6-2, Umegaoka, Aoba-ku,
            Yokohama, Kanagawa 227, Japan (E-mail:watanabe@tcrl.jti.co.jp,
            Tel:045-972-5741)
FEATURES             Location/Qualifiers
     source          1. .2827
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                     /db_xref="taxon:10090"
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                     /db_xref="GI:4176400"
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                     LKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSALRSLRFLQILRMIRMDRRGGTW
                     KLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGENDHFDTYADALWWGLITLT
                     TIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFALKVQEQHRPKHFEKRRN
                     PAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYRLIPPLNQLELLRNLKSKSG
                     LTFRKEPQPEPSPSQKVSLKDRVFSSPRGMAAKGKGSPQAQTVRRSPSADQSLDDSPS
                     KVPKSWSFGDRSRTRQAFRIKGAASRQNSEEASLPGEDIVEDNKSCNCEFVTEDLTPG
                     LKVSIRAVCVMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLSRIKSLQSRVDHIV
                     GRGPTITDKDRTKGPAETELPEDPSMMGRLGKVEKQVLSMEKKLDFLVSIYTQRMGIP
                     PAETEAYFGAKEPEPAPPYHSPEDSRDHADKHGCIIKIVRSTSSTGQRNYAAPPAIPP
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     polyA_site      2827
                     /note="20 a nucleotides"
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BASE COUNT 589 a 830 c 816 g 592 t
ORIGIN

Query Match 19.3%; Score 519.6; DB 10; Length 2827;
Best Local Similarity 58.1%; Pred. No. 6.9e-123;
Matches 1042; Conservative 0; Mismatches 674; Indels 78; Gaps 4;

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Db    153 GGCTTCGTGGGGCTGGACCCCGGCGCGCCCGACTCCACACGCGACGGCGCGCTACTCATC 212

Qy    124 GAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTAC 183
Db    213 GCGGGCTCCGAGGCCCCCAAGCGCGGCAGCGTTTTGAGCAAACCGCGGACGGGCGGCGCG 272

Qy    184 ACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
Db    273 GGAGCCGGGAAGCCCCCGAAGCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCCTCTAC 332

Qy    244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
Db    333 AACGTGCTAGAGCGGCCCCGCGGCTGGGCGTTCATCTACCACGCCTACGTGTTCCTTTTA 392

Qy    304 GTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
Db    393 GTCTTCTCCTGCCTTGTGCTTTCTGTGTTTTCCACCATCAAGGAGTACGAGAAGAGCTCT 452

Qy    364 TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATC 423
Db    453 GAGGGGGCCCTCTACATCTTGGAAATCGTGACTATCGTGGTATTCGGTGTTGAGTACTTT 512

Qy    424 ATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGG 483
Db    513 GTGAGGATCTGGGCTGCAGGCTGCTGTTGCCGGTATCGAGGCTGGAGGGGCAGGCTCAAG 572

Qy    484 TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTT 543
Db    573 TTTGCCAGGAAGCCGTTCTGTGTGATTGATATCATGGTGCTGATTGCCTCCATTGCTGTG 632

Qy    544 GTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGTTTC 603
Db    633 CTGGCTGCTGGTTCCCAGGGCAATGTCTTTGCCACATCTGCGCTTCGGAGCTTGCGGTTC 692

Qy    604 CTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGT 663
Db    693 TTGCAAATCTTGCGGATGATCCGTATGGACCGGAGGGGTGGCACCTGGAAGCTCTTGGGA 752

Qy    664 TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTGGTT 723
Db    753 TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGCCTGGTACATTGGCTTCCTCTGC 812

Qy    724 CTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTTTCT 783
Db    813 CTCATCCTGGCCTCATTTCTGGTGTACTTGGCAGAAAAGGGTGAGAATGACCACTTTGAC 872

Qy    784 ACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGAC 843
Db    873 ACCTACGCAGATGCACTCTGGTGGGGTCTGATCACCCTGACGACCATTGGCTACGGGGAC 932

Qy    844 AAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATT 903
Db    933 AAGTACCCTCAGACCTGGAACGGGAGGCTGCTGGCAGCGACCTTTACCCTCATTGGTGTC 992

Qy    904 TCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAA 963
Db    993 TCGTTCTTTGCTCTTCCTGCTGGCATTTTGGGATCCGGCTTTGCCCTGAAAGTCCAAGAG 1052

Qy    964 CAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGT 1023
Db   1053 CAGCATCGGCCAAAACACTTTGAGAAACGGCGGAACCCTGCGGCAGGTCTGATCCAGTCT 1112
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Qy   1024 GTTTGGCGTAGTTACGCAGCTGATGAGAAAT---------------------------- 1054
          |  |||  |    || ||  || |       |
Db   1113 GCCTGGAGATTCTATGCTACTAACCTCTCACGCACCGACCTGCACTCCACGTGGCAGTAC 1172

Qy   1055 ----------------CTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCAC 1098
                          ||||  ||||    |     |  ||||   ||||     || |
Db   1173 TACGAGCGGACAGTCACTGTCCCCATGTACAGACTCATCCCACCTCTGAACCAGCTGGAG 1232

Qy   1099 ACCTGCAGCCCTACCAAGA--------------------------AAGAACAAGGGGAA 1131
               ||   |  |||||                          |   |||    ||
Db   1233 CTGCTGAGGAATCTCAAGAGCAAATCTGGACTCACCTTCAGGAAGGAGCCACAGCCAGAG 1292

Qy   1132 GCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAG---TGCGCATGGCTAGCCCCAGG 1188
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Db   1293 CCATCACCAAGTCAGAAGGTCAGTTTGAAAGATCGTGTCTTCTCCAGCCCCCGAGGCATG 1352

Qy   1189 GGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGAC 1248
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Qy   1249 ATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACC 1308
             |     || | ||| || | ||| ||||  |||||||||||||    ||||| | |
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Qy   1309 CGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGAC 1368
          |||   || |   |  | ||| ||||  || ||    |   |       ||| |  |
Db   1473 CGCACACGCCAGGCTTTCCGCATCAAGGGTGCTGCATCCCGGCAGAATTCAGAAGAAGCA 1532

Qy   1369 ACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTG 1428
          |    || |||    ||    ||| | ||  | ||  | ||  | || ||  |
Db   1533 AGCCTCCCTGGGGAGGACATCGTAGAGGACAACAAGAGCTGTAACTGCGAGTTTGTGACT 1592

Qy   1429 GAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCAT 1488
          |||||  || |||||    || |||  |  |||  |||||  |  |  |||||   ||
Db   1593 GAAGATCTTACCCCTGGCCTCAAAGTTAGCATCAGAGCTGTGTGTGTTATGCGGTTCTTG 1652

Qy   1489 GTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAA 1548
          ||  | || || ||||| || || |   | || ||||||||||| |  || ||||| |||
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Qy   1549 CAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTT 1608
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Db   1713 CAGTACTCGGCTGGACACTTGGATATGTTGTCCCGCATCAAGAGCCTGCAGTCCAGAGTG 1772

Qy   1609 GATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACA 1668
          || || ||| | ||    || | ||  | | | |||||| |  |||   |||    ||
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          || |||   |||    | || || | ||| ||| | || ||| | |  ||||| || |||
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Qy   1729 CAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAG 1782
          |||||   |||||| ||    ||||| |||| | |  |   |||||||  ||||
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	100.0	2694	22	AAS14652	Human cDNA encodin
2	2694	100.0	2694	24	AAD27192	Human potassium ch
3	2690.4	99.9	3071	22	AAS14651	Human cDNA for vol
4	2689.2	99.8	3137	22	AAC85414	Human KCNQ5 potass
5	2681.2	99.5	3074	22	AAH49499	Human KCNQ5 DNA.
6	2630	97.6	2667	22	AAS14653	Human cDNA encodin
7	2625.2	97.4	2772	22	AAH43633	Human ion-channel

8	2625.2	97.4	3111	22	AAH43634	Human ion-channel
9	2585	96.0	3718	21	AAC64371	Human KCNQ5 (KCN6q
10	963.4	35.8	125910	21	AAC64370	Human KCNQ5 (KCN6q
11	518.4	19.2	2335	21	AAA47618	KCNQ4 Potassium ch
12	516	19.2	2273	20	AAX57140	Mouse KCNQ2 cDNA.
13	510	18.9	2169	20	AAX26588	Nucleotide sequenc
14	480.6	17.8	7413	23	AAS74832	DNA encoding novel
15	477	17.7	2565	20	AAX81548	Human brain-derive
16	477	17.7	3195	23	AAS74831	DNA encoding novel
17	466.6	17.3	3029	20	AAX81547	Human brain-derive

RESULT 1
AAS14652
ID AAS14652 standard; cDNA; 2694 BP.
XX
AC AAS14652;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding a voltage gated potassium channel hKVNQ5-1.
XX
KW Human; ss; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder;
KW stroke; pain; gene therapy; splice variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2994
FT /*tag= a
FT /product= "hKCNQ5-1"
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US09328.
XX
PR 21-MAR-2000; 2000US-190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
DR P-PSDB; AAU09020.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ alpha
PT subunits -
XX
PS Claim 5; Page 62-63; 78pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an
CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
CC sequence and forms a KCNQ potassium channel having the characteristic of
CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
CC included in the scope of the invention are the nucleic acids encoding
CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
CC expression vectors encoding them, antibodies against them, the use of
CC 3-dimensional computer modelling to identify molecules that bind to a
CC KCNQ containing potassium channel and modulate ion flux through the
CC channel. The KCNQ polypeptide is useful for identifying a compound that
CC increases or decreases ion flux through a potassium channel expressed in
CC an eukaryotic host cell or cell membrane. The compound (and the

CC KCNQ nucleic acid when used in gene therapy)is useful as
CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
CC such as disorders of the central nervous system, such as epilepsy,
CC migraines, hearing and vision problems, psychotic disorders, seizures,
CC learning and memory disorders, stroke and pain. The antibodies are
CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
CC use of a nucleotide sequence of KCNQ5 to search computer databases to
CC find variants of the sequence which are associated with disease states,
CC is useful for screening mutations of KCNQ5. The present sequence is
CC a splice variant of hKCNQ5 encoding hKCNQ5-1.
XX
SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 other;

Query Match 100.0%; Score 2694; DB 22; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
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Db 1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy 61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

RESULT 2
AAD27192
ID AAD27192 standard; cDNA; 2694 BP.
XX
AC AAD27192;
XX
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNQ5 cDNA.
XX
KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW learning deficiency; cognitive disorder; motor disease; neuron disease;
KW neurophysiological disorder; neuropsychological disorder; asthma;
KW neuron cell death; brain tumour; gene therapy; antisense therapy;
KW synaptic transmission; electrical excitability; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2694
FT /*tag= a
FT /product= "Human KCNQ5 protein"
XX
PN WO200192526-A1.
XX
PD 06-DEC-2001.
XX
PF 24-MAY-2001; 2001WO-US17314.
XX
PR 26-MAY-2000; 2000US-207389P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Dworetzky SI, Ramanathan CS, Trojnacki JT, Boissard CG;
PI Gribkoff VK;
XX
DR WPI; 2002-122069/16.
DR P-PSDB; AAE16599.
XX

PT Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
PT it, for diagnosing, treating and identifying modulators useful in
PT treating neurological, neurophysiological and neuropsychological
PT diseases -
XX
PS Claim 3; Fig 1; 128pp; English.
XX
CC The invention relates to potassium channel polypeptides referred to
CC as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
CC polypeptides are useful for identifying compounds that modulate their
CC biological activity. The compounds identified and KCNQ5 polynucleotides
CC are useful for treating acute and chronic pain, migraine, acute stroke,
CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis
CC (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
CC disorders, depression, bipolar disorders, sleep disorders, eating
CC disorders, addiction, myokymia, Alzheimer's disease, age-associated
CC memory loss, learning deficiencies, cognitive disorders and motor
CC neuron diseases. The nucleic acid molecules of the invention are
CC further useful for treating neurophysiological, neuropsychological
CC disorders, asthma, neuron cell death and brain tumours. They are also
CC used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate
CC synaptic transmission and electrical excitability in the brain and are
CC useful for generating antibodies. They are also useful to affinity
CC purify biological effectors from biological materials e.g. disease
CC tissues or cells. The present sequence is human KCNQ5 cDNA.
XX
SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 other;

Query Match 100.0%; Score 2694; DB 24; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
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Db       1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy      61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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RESULT 12
AAX57140
ID AAX57140 standard; DNA; 2273 BP.
XX
AC AAX57140;
XX
DT 22-JUL-1999 (first entry)
XX
DE Mouse KCNQ2 cDNA.
XX
KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
KW detection; gene therapy; drug screening; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..2273
FT /*tag= a
FT /product= "KCNQ2"
FT /note= "Partial sequence, no stop codon given"
XX
PN WO9921875-A1.
XX
PD 06-MAY-1999.
XX
PF 23-OCT-1998; 98WO-US22375.
XX

PR 24-OCT-1997; 97US-0063147.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Charlier C, Leppert MF, Singh NA;
XX
DR WPI; 1999-312938/26.
DR P-PSDB; AAY08345.
XX
PT Nucleic acid encoding potassium channels KCNQ2 and 3
XX
PS Claim 1; Page 153-156; 195pp; English.
XX
CC This invention describes novel human and mouse potassium channel proteins
CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC in cell-free form) are used to screen for agents that can be used to
CC treat or prevent these forms of epilepsy. Fragments of the encoding
CC nucleic acids are used as probes or primers, either for detecting
CC mutations or for isolation of related sequences, while the complete
CC sequences may be used in gene therapy to provide wild-type protein.
CC Antibodies specific for mutant or wild-type proteins are used as
CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC useful in rational design of drugs and therapeutically (in replacement
CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC 3 sequences can now be diagnosed early (before symptoms are manifest),
CC and better treatment options will be available.
XX
SQ Sequence 2273 BP; 486 A; 670 C; 653 G; 448 T; 16 other;

Query Match 19.2%; Score 516; DB 20; Length 2273;
Best Local Similarity 57.6%; Pred. No. 1.7e-141;
Matches 1030; Conservative 2; Mismatches 684; Indels 72; Gaps 4;

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Qy     64 GGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTGAGG 123
          ||| |  |  ||||| | || ||| | ||          ||| ||||      || |
Db     67 GGCTTCGTGGGGCTGGACCCCGGCGNGCCCGANTCCACACGCGACGGCNCNCTACTCATC 126

Qy    124 GAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTAC 183
          | | ||  |  || |    || | | |    |         |  |  | || |
Db    127 GCGGGCTCCGAGGCCCCCAAGCGCGGCANCNTNTTGAGCAAGCCGCGGACGGGCGGCGCG 186

Qy    184 ACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
              |  ||  |      ||||||| |   |||||   | ||||||| | ||| |||
Db    187 GGANCCGGGAAGCCCCCNAANCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCCTCTAC 246

Qy    244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
          |||||||| ||| | |||||||||| |||||||||||||||||| | ||| || |||||
Db    247 AACGTGCTAGAGCGGCCCCGCGGCTNGGCGTTCATCTACCACGCCTACGTGTTCCTCCTG 306

Qy    304 GTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
          || ||    ||| |  |  | || |||||||| ||||||   ||| ||   ||     |
Db    307 GTTTTCTCCTGCCTTGTGCTTTCTGTGTTTTCCACCATCAAGGAGTACGAGAAGAGCTCT 366

Qy    364 TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATC 423
             |  |||||  ||| ||||  ||||||  || || || || ||| | |||| | |
Db    367 GAGGGGGCCCTCTACATCTTGGAAATCGTGACTATCGTGGTATTCGGTGTTGAGTACTTT 426

Qy    424 ATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGG 483
           |  | |||||| |||| || |||||||| || ||| |||| |||   || || || | |
Db    427 GTGAGGATCTGGGCTGCAGGCTGCTGTTGCCGGTATCGAGGCTGGAGGGGCAGGCTCAAG 486

Qy    484 TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTT 543
          |||||  | ||||| |||||||| || |||| ||| || || || || || || || ||
Db    487 TTTGCCAGGAAGCCGTTCTGTGTGATTGATATCATGGTGCTGATTGCCTCCATTGCTGTG 546

Qy    544 GTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGTTTC 603
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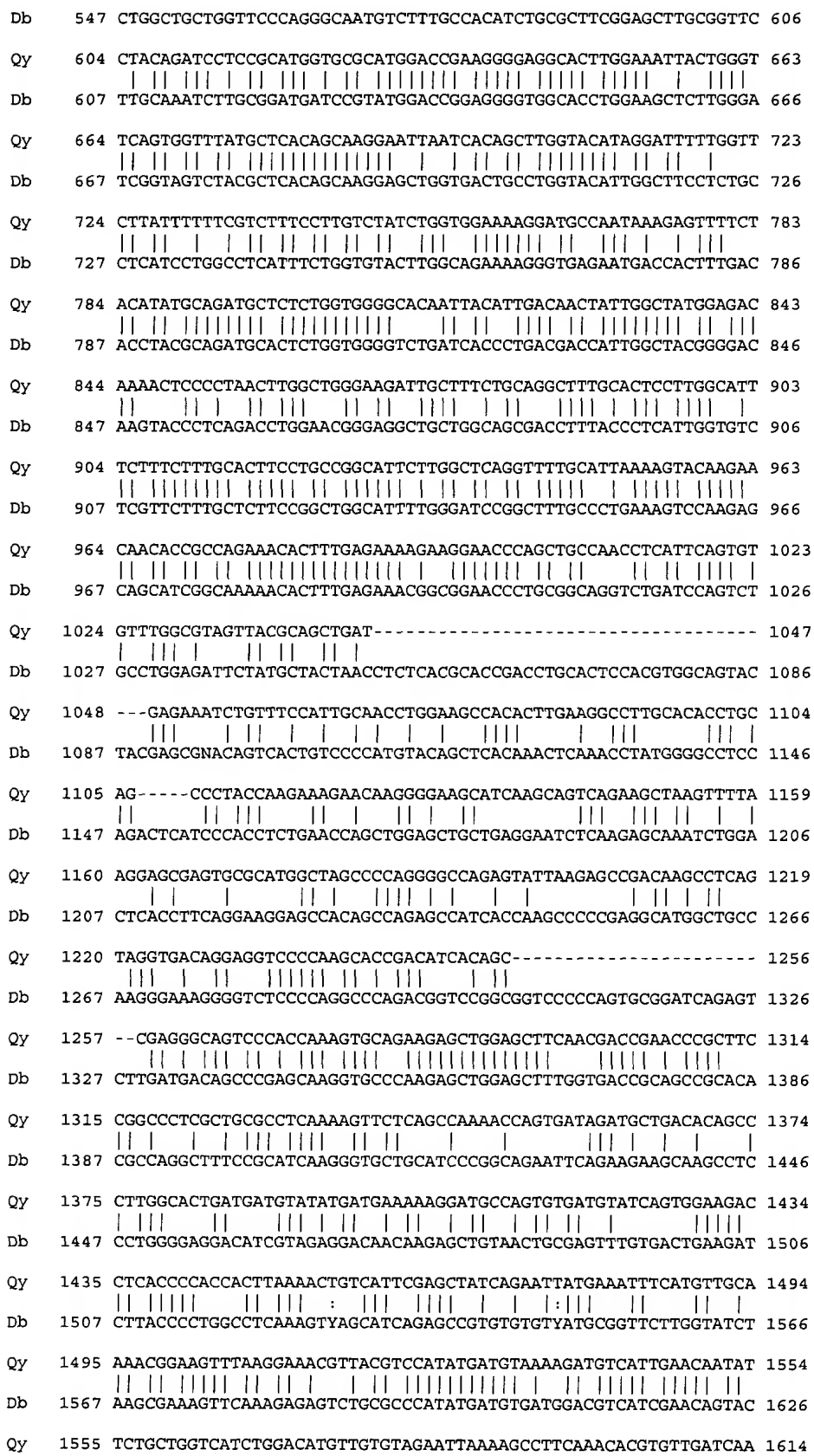

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Qy   1615 ATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAA 1674
          ||| | ||    || | ||  | | | |||||| |    ||    |||    |||| |||
Db   1687 ATTGTGGGGCGGGGCCCAACAATAACGGATAAGGA---TCGCACCAAAGGCCCAGCGGAA 1743

Qy   1675 CATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTA 1734
             |||    | || || | ||| ||| | || ||| | |  ||||| || ||||||||
Db   1744 ACGGAGCTGCCCGAAGACCCCAGCATGATGGGACGGCTTGGGAAGGTGGAGAAACAGGTC 1803

Qy   1735 CAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAG 1782
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Db   1804 TTGTCCATGGAAAAGAAGCTCGACTTCTTGGTGAGCATCTATACACAG 1851
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	600.2	22.3	658	10	BE158938	BE158938 MR0-HT040
2	553.8	20.6	734	12	BG532543	BG532543 602562103
3	549.4	20.4	632	10	BB624101	BB624101 BB624101
4	536.4	19.9	547	13	BI034993	BI034993 QV2-NN200
c 5	530.8	19.7	570	13	BI033850	BI033850 QV2-NN200
c 6	524.4	19.5	679	10	BE647997	BE647997 UI-M-BH1-
7	522	19.4	908	12	BF240146	BF240146 601905649
8	516.8	19.2	584	10	AW049888	AW049888 UI-M-BH1-
c 9	487.4	18.1	506	12	BF959996	BF959996 QV2-NN004
10	474	17.6	491	12	BF959488	BF959488 QV2-NN004
11	454.8	16.9	997	10	BB609854	BB609854 BB609854
c 12	415.8	15.4	435	12	BF943257	BF943257 QV2-NN004
13	414.6	15.4	469	10	BE103175	BE103175 UI-R-BT1-
14	403	15.0	517	12	BF954375	BF954375 QV2-NN004
15	400.8	14.9	568	14	BQ339931	BQ339931 QV2-NN004
c 16	378.4	14.0	477	17	AZ443500	AZ443500 1M0238H18
c 17	354.6	13.2	434	13	BI290441	BI290441 UI-R-DK0-
18	339.8	12.6	528	12	BG732557	BG732557 333306 MA
c 19	310.8	11.5	427	12	BF523361	BF523361 UI-R-G0-u
20	302.2	11.2	914	12	BF312386	BF312386 601898926
21	301.4	11.2	515	12	BF962769	BF962769 QV2-NN004

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RESULT 8
AW049888
LOCUS       AW049888                584 bp    mRNA    linear   EST 18-SEP-1999
DEFINITION  UI-M-BH1-anr-g-09-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
            UI-M-BH1-anr-g-09-0-UI 3', mRNA sequence.
ACCESSION   AW049888
VERSION     AW049888.1  GI:5910417
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 584)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            Oligo-dT track not found, Not I site shown in beginning of sequence
```

is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 37-71, >GC_rich#Low_complexity
Seq primer: M13 Forward
POLYA=No.

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                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S2 library is a subtracted library derived from
                     NIH_BMAP_M_S1, which in turn is a subtracted library
                     derived from a mixture of normalized libraries from ten
                     regions of the mouse brain (cerebellum, brain stems,
                     olfactory bulbs, hypothalamus, cortex, amygdala, basal
                     ganglia, pineal gland, striatum, hipoccampus). The driver
                     used for subtraction consisted of a pool of 5,000 clones
                     from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
                     obtained from non-normalized and normalized mouse brain
                     spinal cord libraries.
                     TAG_LIB=NIH_BMAP_M_S2
                     TAG_TISSUE=corpus-striatum
                     TAG_SEQ=ACGGC"
BASE COUNT      107 a    151 c    174 g    152 t
ORIGIN

  Query Match             19.2%;  Score 516.8;  DB 10;  Length 584;
  Best Local Similarity   92.8%;  Pred. No. 2.9e-116;
  Matches  542;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy      47 CAGCCGCCAGGGGCGACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCG 106
           | ||||||||||||||||||||||  |||| ||||||||||||||  |||| || || |
Db       1 CGGCCGCCAGGGGCGACGGCCTGCTGTTGCTCGGCACCCGCGCGGCGGCGCTCGGCGGAG 60

Qy     107 GCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGG 166
           ||||||| ||| |||| |||||||||||||||||||||||||||||| ||||||||||||
Db      61 GCGGCGGCGGCTTGAGAGAGAGCCGCCGGGGCAAGCAGGGGGCCCGAATGAGCCTGCTGG 120

Qy     167 GGAAGCCGCTCTCTTACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGG 226
           |||||||||||||| ||||| || |||||||||| ||||||||||||||||||||||||||
Db     121 GGAAGCCGCTCTCCTACACCAGCAGCCAGAGCTGTCGGCGCAACGTCAAGTACCGGCGGG 180

Qy     227 TGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACG 286
           |||||||||| |||||||||||||||||| |||||||||||||||||||| |||||||||
Db     181 TGCAGAACTATCTGTACAACGTGCTGGAGCGACCCCGCGGCTGGGCGTTCGTCTACCACG 240

Qy     287 CTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTG 346
           | ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     241 CGTTCGTTTTTCTCCTTGTGTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTG 300

Qy     347 AGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCT 406
           ||||  |||||||||||  |||||||||||||| || |||||||||||||||| || ||||
Db     301 AGCATACAAAATTGGCTTCAAGTTGCCTCTTAATTCTGGAGTTCGTGATGATCGTTGTCT 360

Qy     407 TTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGAT 466
           ||||  |||||||||||||||||||||||||||| ||||||||||||| ||||||||||
Db     361 TTGGCTTGGAGTTCATCATTCGAATCTGGTCTGCAGGTTGCTGTTGTCGTTATAGAGGAT 420

Qy     467 GGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTA 526
           |||||||||||||||||||||||||||| || |||||||| |||||||||||||||| |
Db     421 GGCAAGGAAGACTGAGGTTTGCTCGAAAACCATTCTGTGTAATAGATACCATTGTTCTCA 480
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Qy     527 TCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCAC 586
           |||||||||||||||||| |||||||||||||||||||||||| |||||||| || |
Db     481 TCGCTTCAATAGCAGTTGTCTCTGCAAAAACTCAGGGTAATATTTTCGCCACGTCAGCGC 540

Qy     587 TCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATG 630
           |||||||||||||| |||||||||||||| || ||||||||||||
Db     541 TCAGAAGTCTCCGGTTCCTACAGATCCTGCGTATGGTGCGCATG 584
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SEQ ID NO: 2

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1813	39.5	722	4	US-09-105-058C-23	Sequence 23, Appl
2	1801	39.3	930	4	US-09-177-650-96	Sequence 96, Appl
3	1800	39.2	871	4	US-09-105-058C-20	Sequence 20, Appl
4	1795.5	39.1	872	4	US-09-177-650-2	Sequence 2, Appli
5	1763.5	38.4	757	4	US-09-177-650-89	Sequence 89, Appl
6	1611	35.1	854	4	US-09-105-058C-27	Sequence 27, Appl
7	1611	35.1	872	4	US-09-177-650-7	Sequence 7, Appli
8	1560	34.0	870	4	US-09-177-650-91	Sequence 91, Appl
9	1207.5	26.3	300	4	US-09-105-058C-4	Sequence 4, Appli
10	1207.5	26.3	300	4	US-09-105-058C-6	Sequence 6, Appli
11	1186.5	25.9	807	4	US-09-177-650-3	Sequence 3, Appli
12	1102.5	24.0	676	4	US-09-135-021-2	Sequence 2, Appli
13	1102.5	24.0	676	4	US-09-135-020-2	Sequence 2, Appli
14	1102.5	24.0	676	4	US-09-135-010A-2	Sequence 2, Appli
15	1102.5	24.0	676	4	US-09-444-871-2	Sequence 2, Appli
16	1102.5	24.0	676	4	US-09-634-920-2	Sequence 2, Appli

RESULT 1
US-09-105-058C-23
; Sequence 23, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 722
; TYPE: PRT
; ORGANISM: mouse
US-09-105-058C-23

Query Match 39.5%; Score 1813; DB 4; Length 722;
Best Local Similarity 55.5%; Pred. No. 5.4e-156;
Matches 393; Conservative 72; Mismatches 153; Indels 90; Gaps 17;

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           : |   ||: |: |      | | : | |  ||     |||         :||  ||::
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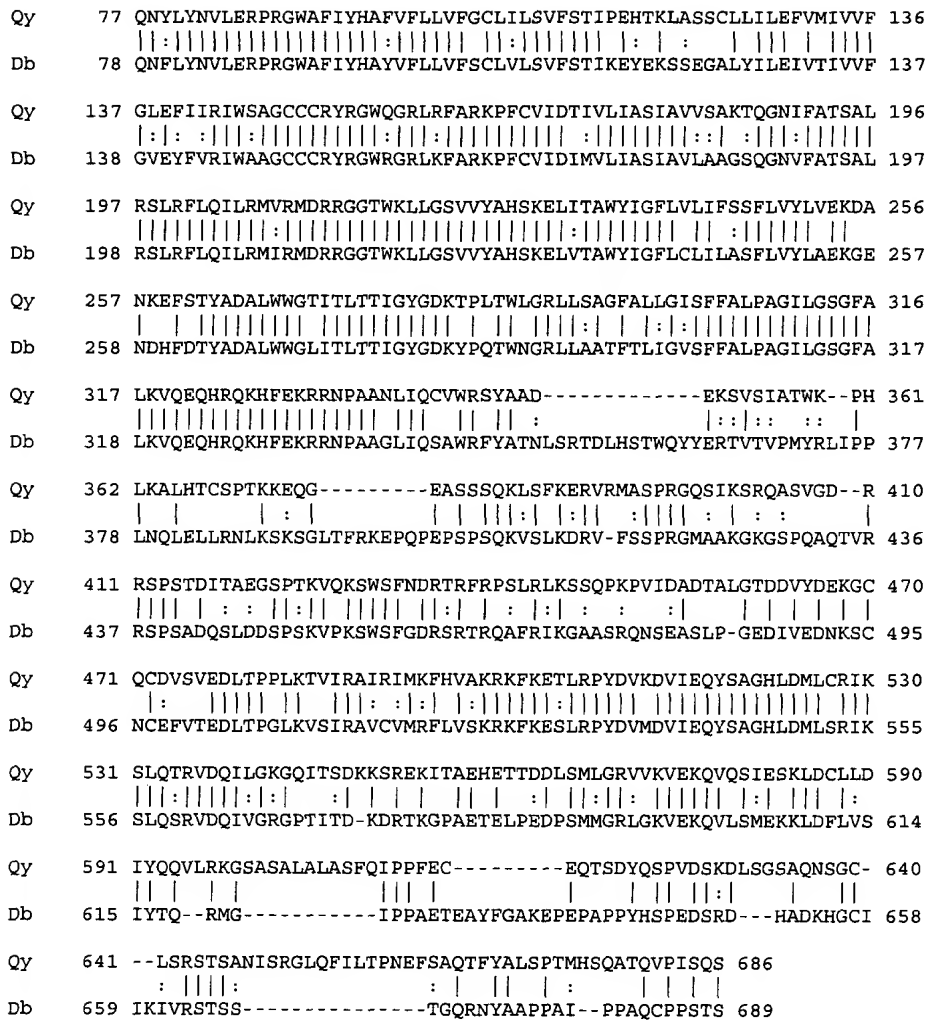

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	4588	100.0	897	22	AAB47046	Human KCNQ5 potass
3	4588	100.0	897	23	AAE16599	Human potassium ch
4	4585	99.9	897	22	AAU09023	Human voltage gate
5	4585	99.9	897	22	AAU09025	Human voltage gate
6	4584	99.9	897	22	AAU09024	Human voltage gate
7	4582	99.9	897	22	AAU09022	Human voltage gate
8	4574	99.7	932	22	AAB86979	Human KCNQ5 protei
9	4527.5	98.7	888	22	AAU09021	Human voltage gate
10	4527.5	98.7	923	22	AAB47678	Human ion-channel
11	4330	94.4	846	21	AAB24241	Human KCNQ5 (KCN6q
12	1989.5	43.4	695	21	AAB01476	KCNQ4 Potassium ch
13	1989.5	43.4	695	23	AAE16621	Human potassium ch
14	1814.5	39.5	844	23	AAE16619	Human potassium ch
15	1813	39.5	722	20	AAY01530	Amino acid sequenc
16	1807.5	39.4	854	20	AAY23215	Human brain-derive
17	1807.5	39.4	912	22	ABG10644	Novel human diagno

RESULT 1
AAU09020
ID AAU09020 standard; Protein; 897 AA.
XX
AC AAU09020;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human voltage gated potassium channel hKVNQ5-1.
XX
KW Human; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder;
KW stroke; pain; gene therapy; splice variant.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Region   343..640
FT   /label= Conserved_region
FT   /note= "This sequence is specifically claimed in
FT   claim 13"
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US09328.
XX
PR 21-MAR-2000; 2000US-190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
DR N-PSDB; AAS14652.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ alpha
PT subunits -
XX
PS Claim 17; Page 64; 78pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an
CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
CC sequence and forms a KCNQ potassium channel having the characteristic of
CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
CC included in the scope of the invention are the nucleic acids encoding
CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
CC expression vectors encoding them, antibodies against them, the use of
CC 3-dimensional computer modelling to identify molecules that bind to a
CC KCNQ containing potassium channel and modulate ion flux through the
CC channel. The KCNQ polypeptide is useful for identifying a compound that
CC increases or decreases ion flux through a potassium channel expressed in
CC an eukaryotic host cell or cell membrane. The compound (and the
CC KCNQ nucleic acid when used in gene therapy)is useful as
CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
CC such as disorders of the central nervous system, such as epilepsy,
CC migraines, hearing and vision problems, psychotic disorders, seizures,
CC learning and memory disorders, stroke and pain. The antibodies are
CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
CC use of a nucleotide sequence of KCNQ5 to search computer databases to
CC find variants of the sequence which are associated with disease states,
CC is useful for screening mutations of KCNQ5. The present sequence is
CC encoded by a splice variant of hKCNQ5 and is hKCNQ5-1.
XX

SQ Sequence 897 AA;

Query Match 100.0%; Score 4588; DB 22; Length 897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
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Db       1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy      61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy     121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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Db     121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy     181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy     241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy     301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
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Db     301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy     361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy     421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy     481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy     541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy     601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy     661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy     721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy     781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy     841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
```

RESULT 2
AAB47046
ID AAB47046 standard; Protein; 897 AA.
XX

AC AAB47046;
XX
DT 20-APR-2001 (first entry)
XX
DE Human KCNQ5 potassium channel subunit.
XX
KW Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
KW central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
KW CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
KW compulsive behaviour; dementia; depression; Huntington's disease;
KW mania; memory impairment; memory dysfunction; spinal cord damage;
KW phobia; pick's disease; psychosis; stroke; tremor; seizure; convulsion;
KW epilepsy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 93..0
FT /label= Site 1
FT Binding-site 120..138
FT /label= Site 2
FT Binding-site 166..185
FT /label= Site 3
FT Binding-site 188..213
FT /label= Site 4
FT Binding-site 230..252
FT /label= Site 5
FT Region 265..284
FT /label= P-loop
FT Binding-site 291..314
FT /label= Site 6
FT Domain 495..544
FT /label= A-domain
XX
PN WO200077035-A2.
XX
PD 21-DEC-2000.
XX
PF 29-MAY-2000; 2000WO-DK00289.
XX
PR 11-JUN-1999; 99DK-0000828.
XX
PA (NEUR-) NEUROSEARCH AS.
XX
PI Jentsch TJ;
XX
DR WPI; 2001-080678/09.
DR N-PSDB; AAC85414.
XX
PT Novel genes encoding KCNQ5 potassium channel subunits, useful for
PT treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,
PT depression, Huntington's disease, schizophrenia and Parkinson's disease
PT -
XX
PS Claim 8; Page 48-50; 50pp; English.
XX
CC This sequence shows the human KCNQ5 protein. The KCNQ5 protein forms
CC heteromeric channels with other KCNQ channel subunits, in particular
CC KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
CC chromosome 6 (6q14). Chemicals which have the ability to bind to
CC KCNQ5 are useful for diagnosis, treatment, prevention or alleviation
CC of diseases related to diseases or adverse conditions of the central
CC nervous system (CNS), including affective disorders, Alzheimer's
CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
CC neurodegenerative illness, cognitive deficits, compulsive behavior,
CC dementia, depression, Huntington's disease, mania, memory impairment,
CC memory disorders, memory dysfunction, motion disorders, motor
CC disorders, neurodegenerative diseases, Parkinson's disease and
CC Parkinson-like motor disorders, phobias, pick's disease, psychosis,
CC schizophrenia, spinal cord damage, stroke, tremor, seizures,
CC convulsions and epilepsy.

XX
SQ Sequence 897 AA;

Query Match 100.0%; Score 4588; DB 22; Length 897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy      61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy     121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy     181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy     241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy     301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy     361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy     421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy     481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy     541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy     601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy     661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy     721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy     781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy     841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
```

RESULT 3

AAE16599
ID AAE16599 standard; Protein; 897 AA.
XX
AC AAE16599;
XX
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNQ5.
XX
KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW learning deficiency; cognitive disorder; motor disease; neuron disease;
KW neurophysiological disorder; neuropsychological disorder; asthma;
KW neuron cell death; brain tumour; gene therapy; antisense therapy;
KW synaptic transmission; electrical excitability.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 191..209
FT /note= "Pore region"
FT Region 265..285
FT /note= "S4 voltage sensor region"
XX
PN WO200192526-A1.
XX
PD 06-DEC-2001.
XX
PF 24-MAY-2001; 2001WO-US17314.
XX
PR 26-MAY-2000; 2000US-207389P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Dworetzky SI, Ramanathan CS, Trojnacki JT, Boissard CG;
PI Gribkoff VK;
XX
DR WPI; 2002-122069/16.
DR N-PSDB; AAD27192.
XX
PT Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
PT it, for diagnosing, treating and identifying modulators useful in
PT treating neurological, neurophysiological and neuropsychological
PT diseases -
XX
PS Claim 25; Fig 2; 128pp; English.
XX
CC The invention relates to potassium channel polypeptides referred to
CC as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
CC polypeptides are useful for identifying compounds that modulate their
CC biological activity. The compounds identified and KCNQ5 polynucleotides
CC are useful for treating acute and chronic pain, migraine, acute stroke,
CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis
CC (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
CC disorders, depression, bipolar disorders, sleep disorders, eating
CC disorders, addiction, myokymia, Alzheimer's disease, age-associated
CC memory loss, learning deficiencies, cognitive disorders and motor
CC neuron diseases. The nucleic acid molecules of the invention are
CC further useful for treating neurophysiological, neuropsychological
CC disorders, asthma, neuron cell death and brain tumours. They are also
CC used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate
CC synaptic transmission and electrical excitability in the brain and are
CC useful for generating antibodies. They are also useful to affinity
CC purify biological effectors from biological materials e.g. disease
CC tissues or cells. The present sequence is human KCNQ5 protein.
XX
SQ Sequence 897 AA;

```
  Query Match             100.0%;  Score 4588;  DB 23;  Length 897;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  897;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy      61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy     121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy     181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy     241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy     301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy     361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy     421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy     481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy     541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy     601 ASALALASFQIPPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ASALALASFQIPPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy     661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy     721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy     781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy     841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
```

RESULT 15
AAY01530
ID AAY01530 standard; Protein; 722 AA.

XX
AC AAY01530;
XX
DT 16-JUN-1999 (first entry)
XX
DE Amino acid sequence of murine KCNQ2/KvLR1.
XX
KW KCNQ protein; nervous system-specific potassium channel;
KW neuronal excitability; neurotransmitter release; KCNQ modulator;
KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
KW age-associated memory loss; learning deficiency; motor neuron disease;
KW epilepsy; stroke.
XX
OS Mus sp.
XX
PN WO9907832-A1.
XX
PD 18-FEB-1999.
XX
PF 26-JUN-1998; 98WO-US13276.
XX
PR 12-AUG-1997; 97US-0055599.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Blanar MA, Dworetzky S, Gribkoff VK, Levesque PC;
PI Little WA, Neubauer MG, Yang W;
XX
DR WPI; 1999-190047/16.
DR N-PSDB; AAX26588.
XX
PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in
PT neurotransmission and neuroprotection, used to treat, e.g. ataxia
XX
PS Claim 4; Fig 10A-D; 64pp; English.
XX
CC The present sequence represents murine KCNQ2/KvLR1. KCNQ proteins are
CC nervous system-specific potassium channels. In neurons, potassium
CC channels regulate neuronal excitability, action potential shape
CC and firing pattern, and neurotransmitter release. KCNQ modulators
CC may be used to treat disorders such as ataxia, myokymia, seizures,
CC Alzheimer's disease, Parkinson's disease, age-associated memory
CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
CC stroke.
XX
SQ Sequence 722 AA;

Query Match 39.5%; Score 1813; DB 20; Length 722;
Best Local Similarity 55.5%; Pred. No. 2e-152;
Matches 393; Conservative 72; Mismatches 153; Indels 90; Gaps 17;

```
Qy     17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
          : |   ||: |: |      |  | : | |  ||     |||         :||  ||::
Db     34 STRDGALLIAGSEAPK---RGSVLSKPRTGGAGA-----GKP--------PKRNAFYRKL 77

Qy     77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
          ||:||||||||||||||||:|||||| ||:||||||| |: | :   | ||| | ||||
Db     78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy    137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
          |:|: :|||:|||||||||||:|||:|||||||||| :||||||||::| :|||:||||||
Db    138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy    197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
          ||||||||||:|||||||||||||||||||||:||||||| || :|||||| ||
Db    198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy    257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
          |  | |||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||
Db    258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317
```

```
Qy    317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD------------EKSVSIATWK--PH 361
          |||||||||||||||||||| |||  || || :             |::|::  ::  |
Db    318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYRLIPP 377

Qy    362 LKALHTCSPTKKEQG---------EASSSQKLSFKERVRMASPRGQSIKSRQASVGD--R 410
          |  |      | : |         | | |||:| |:||  :|||| : | : :      |
Db    378 LNQLELLRNLKSKSGLTFRKEPQPEPSPSQKVSLKDRV-FSSPRGMAAKGKGSPQAQTVR 436

Qy    411 RSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGC 470
          |||| | : : ||:|| ||||| ||:| | : |:| :  :   :|    | | | | | |
Db    437 RSPSADQSLDDSPSKVPKSWSFGDRSRTRQAFRIKGAASRQNSEASLP-GEDIVEDNKSC 495

Qy    471 QCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIK 530
           |:   ||||| ||  |||: :|:| |:||||||:|||||| |||||||||||||| |||
Db    496 NCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLSRIK 555

Qy    531 SLQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLD 590
          |||:|||||:|:|   :| | | |  || |  :| ||:||: |||||| |:| ||| |:
Db    556 SLQSRVDQIVGRGPTITD-KDRTKGPAETELPEDPSMMGRLGKVEKQVLSMEKKLDFLVS 614

Qy    591 IYQQVLRKGSASALALASFQIPPFEC---------EQTSDYQSPVDSKDLSGSAQNSGC- 640
          || |  | |           ||| |          |    | || ||:|    |   ||
Db    615 IYTQ--RMG-----------IPPAETEAYFGAKEPEPAPPYHSPEDSRD---HADKHGCI 658

Qy    641 --LSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQS 686
            : ||||:               : |  ||  | :     | | | |
Db    659 IKIVRSTSS--------------TGQRNYAAPPAI--PPAQCPPSTS 689
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1226.5	26.7	393	2	JC5275	voltage-gated pota
2	1220.5	26.6	744	2	T34116	voltage-gated pota
3	951.5	20.7	645	2	T27186	hypothetical prote
4	424	9.2	664	2	T28852	probable potassium
5	290	6.3	858	2	S31761	potassium channel
6	285.5	6.2	853	1	CHRTD1	potassium channel
7	279.5	6.1	857	2	I56529	potassium channel
8	276.5	6.0	802	2	JH0595	potassium channel
9	252.5	5.5	581	2	S17150	potassium channel

RESULT 1
JC5275
voltage-gated potassium channel protein - human
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999
C;Accession: JC5275
R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific genes through compiled expression profiles.
A;Reference number: JC5272; MUID:97191543; PMID:9039501
A;Contents: neuroblastma cell
A;Accession: JC5275
A;Molecule type: mRNA
A;Residues: 1-393 <YOK>
A;Cross-references: DDBJ:D82346; NID:g1841341; PIDN:BAA11557.1; PID:d1012224; PID:g1841342

Query Match 26.7%; Score 1226.5; DB 2; Length 393;
Best Local Similarity 69.2%; Pred. No. 1.1e-73;
Matches 238; Conservative 33; Mismatches 56; Indels 17; Gaps 4;

```
Qy     17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
          : |   ||: |: |       |  | : | |  ||     |||          :||  ||::
Db     34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP--------PKRNAFYRKL 77
```

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Qy      77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
           ||:||||||||||||||||:|||||| ||:||||||| |: | :   | ||| | ||||
Db      78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy     137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
           |:|: :|||:||||||||||:|||:|||||||||| :|||||||::| :|||:||||||
Db     138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy     197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
           ||||||||||:|||||||||||||||||||||:|||||||| || :|||||| ||
Db     198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy     257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
           |  | |||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||
Db     258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy     317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSI-ATWK 359
           |||||||||||||||||| |||  || || :     : :||:
Db     318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQ 361
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4588	100.0	897	1	CIQ5_HUMAN	Q9nr82 homo sapien
2	4288	93.5	878	1	CIQ5_MOUSE	Q9jk45 mus musculu
3	1989.5	43.4	695	1	CIQ4_HUMAN	P56696 homo sapien
4	1826	39.8	852	1	CIQ2_RAT	O88943 rattus norv
5	1795.5	39.1	872	1	CIQ2_HUMAN	O43526 homo sapien
6	1776.5	38.7	759	1	CIQ2_MOUSE	Q9z351 mus musculu
7	1611	35.1	872	1	CIQ3_HUMAN	O43525 homo sapien
8	1577	34.4	873	1	CIQ3_RAT	O88944 rattus norv
9	1571	34.2	866	1	CIQ3_BOVIN	P58126 bos taurus
10	1102.5	24.0	676	1	CIQ1_HUMAN	P51787 homo sapien
11	1100	24.0	604	1	CIQ1_MOUSE	P97414 mus musculu

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RESULT 1
CIQ5_HUMAN
ID   CIQ5_HUMAN     STANDARD;      PRT;   897 AA.
AC   Q9NR82; Q9NRN0; Q9NYA6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Voltage-gated potassium channel protein KQT-like 5.
GN   KCNQ5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=20357367; PubMed=10787416;
RA   Lerche C., Scherer C.R., Seebohm G., Derst C., Wei A.D., Busch A.E.,
RA   Steinmeyer K.;
RT   "Molecular cloning and functional expression of KCNQ5, a potassium
RT   channel subunit that may contribute to neuronal M-current
RT   diversity.";
RL   J. Biol. Chem. 275:22395-22400(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC   TISSUE=Brain;
RX   MEDLINE=20379054; PubMed=10816588;
RA   Schroeder B.C., Hechenberger M., Weinreich F., Kubisch C.,
RA   Jentsch T.J.;
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RT "KCNQ5, a novel potassium channel broadly expressed in brain, mediates
RT M-type currents.";
RL J. Biol. Chem. 275:24089-24095(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Kananura C., Biervert B., Hechenberger M., Engels H., Steinlein O.K.;
RT "The new voltage gated potassium channel KCNQ5 and early infantile
RT convulsions.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE OF 37-897 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Retina;
RA Kniazeva M., Han M.;
RT "A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5,
RT is a candidate gene for retinal disorders.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
RX MEDLINE=21095345; PubMed=11159685;
RA Wickenden A.D., Zou A., Wagoner P.K., Jegla T.;
RT "Characterization of KCNQ5/Q3 potassium channels expressed in
RT mammalian cells.";
RL Br. J. Pharmacol. 132:381-384(2001).
CC -!- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
CC EXCITABILITY. ASSOCIATES WITH KCNQ3 TO FORM A POTASSIUM CHANNEL
CC WHICH CONTRIBUTES TO M-TYPE CURRENT, A SLOWLY ACTIVATING AND
CC DEACTIVATING POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN
CC DETERMINING THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS.
CC MAY CONTRIBUTE, WITH OTHER POTASSIUM CHANNELS, TO THE MOLECULAR
CC DIVERSITY OF AN HETEROGENEOUS POPULATION OF M-CHANNELS, VARYING IN
CC KINETIC AND PHARMACOLOGICAL PROPERTIES, WHICH UNDERLY THIS
CC PHYSIOLOGICALLY IMPORTANT CURRENT. INSENSITIVE TO
CC TETRAETHYLAMMONIUM, BUT INHIBITED BY BARIUM, LINOPIRDINE AND
CC XE991. ACTIVATED BY NIFLUMIC ACID AND THE ANTICONVULSANT
CC RETIGABINE. MUSCARINE SUPPRESSES KCNQ5 CURRENT IN XENOPUS OOCYTES
CC IN WHICH CLONED KCNQ5 CHANNELS WERE COEXPRESSED WITH M(1)
CC MUSCARINIC RECEPTORS.
CC -!- SUBUNIT: HETEROMULTIMER WITH KCNQ3.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; ISOFORM 1 (SHOWN HERE), 2 AND 3;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN AND SKELETAL
CC MUSCLE. IN BRAIN, EXPRESSED IN CEREBRAL CORTEX, OCCIPITAL POLE,
CC FRONTAL LOBE AND TEMPORAL LOBE. LOWER LEVELS IN HIPPOCAMPUS AND
CC PUTAMEN. LOW TO UNDETECTABLE LEVELS IN MEDULLA, CEREBELLUM AND
CC THALAMUS.
CC -!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
CC SUBFAMILY.

DR EMBL; AF249278; AAF91335.1; ALT_INIT.
DR EMBL; AF202977; AAF69797.1; -.
DR EMBL; AJ272506; CAC88112.1; -.
DR EMBL; AJ272507; CAC88112.1; JOINED.
DR EMBL; AJ272508; CAC88112.1; JOINED.
DR EMBL; AJ272509; CAC88112.1; JOINED.
DR EMBL; AJ272510; CAC88112.1; JOINED.
DR EMBL; AJ272511; CAC88112.1; JOINED.
DR EMBL; AJ272512; CAC88112.1; JOINED.
DR EMBL; AJ272513; CAC88112.1; JOINED.
DR EMBL; AJ272514; CAC88112.1; JOINED.

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DR   EMBL; AJ272515; CAC88112.1; JOINED.
DR   EMBL; AJ272516; CAC88112.1; JOINED.
DR   EMBL; AJ272517; CAC88112.1; JOINED.
DR   EMBL; AJ272518; CAC88112.1; JOINED.
DR   EMBL; AJ272519; CAC88112.1; JOINED.
DR   EMBL; AF263835; AAF73446.1; -.
DR   HSSP; Q54397; 1BL8.
DR   Genew; HGNC:6299; KCNQ5.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003946; KCNQ1_channel.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR000636; M+channel_nlg.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF03520; KCNQ1_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Multigene family; Alternative splicing.
FT   TRANSMEM     91    111       SEGMENT S1 (POTENTIAL).
FT   TRANSMEM    122    142       SEGMENT S2 (POTENTIAL).
FT   TRANSMEM    166    186       SEGMENT S3 (POTENTIAL).
FT   TRANSMEM    195    217       SEGMENT S4 (POTENTIAL).
FT   TRANSMEM    232    252       SEGMENT S5 (POTENTIAL).
FT   DOMAIN      264    284       SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT   TRANSMEM    291    311       SEGMENT S6 (POTENTIAL).
FT   VARSPLIC    372    381       KKEQGEASSS -> N (IN ISOFORM 2).
FT   VARSPLIC    372    381       KKEQGEASSS -> NKFCSNKQKLFRMYTSRKQS (IN
FT                                ISOFORM 3).
FT   CONFLICT     57     58       KP -> SR (IN REF. 1).
FT   CONFLICT     94     94       Y -> H (IN REF. 4).
FT   CONFLICT    692    692       A -> V (IN REF. 4).
FT   CONFLICT    764    764       T -> P (IN REF. 4).
FT   CONFLICT    822    822       S -> R (IN REF. 4).
FT   CONFLICT    874    874       R -> Q (IN REF. 4).
SQ   SEQUENCE   897 AA;  99024 MW;  0FD7C7731C1D8D11 CRC64;

  Query Match            100.0%;  Score 4588;  DB 1;  Length 897;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-254;
  Matches  897;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy      61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy     121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy     181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy     241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy     301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy     361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy     421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480
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Qy    481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy    541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy    601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy    661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy    721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy    781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy    841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
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RESULT 3
CIQ4_HUMAN
ID   CIQ4_HUMAN     STANDARD;      PRT;   695 AA.
AC   P56696; O96025;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Voltage-gated potassium channel protein KQT-like 4.
GN   KCNQ4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT DFNA2 SER-285.
RC   TISSUE=Retina;
RX   MEDLINE=99148276; PubMed=10025409;
RA   Kubisch C., Schroeder B.C., Friedrich T., Luetjohann B.,
RA   El-Amraoui A., Marlin S., Petit C., Jentsch T.J.;
RT   "KCNQ4, a novel potassium channel expressed in sensory outer hair
RT   cells, is mutated in dominant deafness.";
RL   Cell 96:437-446(1999).
RN   [2]
RP   INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX   MEDLINE=20178300; PubMed=10713961;
RA   Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
RA   Brown D.A.;
RT   "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
RT   via M1 muscarinic acetylcholine receptors.";
RL   J. Physiol. (Lond) 522:349-355(2000).
RN   [3]
RP   PHARMACOLOGICAL CHARACTERIZATION, AND POSSIBLE FUNCTION.
RX   MEDLINE=21143874; PubMed=11245603;
RA   Soegaard R., Ljungstroem T., Pedersen K.A., Oelesen S.-P.,
RA   Jensen B.S.;
RT   "KCNQ4 channels expressed in mammalian cells: functional
RT   characteristics and pharmacology.";
RL   Am. J. Physiol. 280:C859-C866(2001).
RN   [4]
RP   VARIANTS DFNA2 SER-276; CYS-285 AND SER-321.
RX   MEDLINE=99299248; PubMed=10369879;
```

```
RA   Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schatteman I.,
RA   Van Velzen D., Meyers J., Ensink R.J., Verstreken M., Declau F.,
RA   Marres H., Kastury K., Bhasin S., McGuirt W.T., Smith R.J.H.,
RA   Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.,
RA   Van Camp G.;
RT   "Mutations in the KCNQ4 gene are responsible for autosomal dominant
RT   deafness in four DFNA2 families.";
RL   Hum. Mol. Genet. 8:1321-1328(1999).
RN   [5]
RP   VARIANT DFNA2 SER-281.
RX   MEDLINE=20040027; PubMed=10571947;
RA   Talebizadeh Z., Kelley P.M., Askew J.W., Beisel K.W., Smith S.D.;
RT   "Novel mutation in the KCNQ4 gene in a large kindred with dominant
RT   progressive hearing loss.";
RL   Hum. Mutat. 14:493-501(1999).
RN   [6]
RP   VARIANT DFNA2 HIS-274.
RX   MEDLINE=20388752; PubMed=10925378;
RA   Van Hauwe P., Coucke P.J., Ensink R.J., Huygen P., Cremers C.W.R.J.,
RA   Van Camp G.;
RT   "Mutations in the KCNQ4 K+ channel gene, responsible for autosomal
RT   dominant hearing loss, cluster in the channel pore region.";
RL   Am. J. Med. Genet. 93:184-187(2000).
CC   -!- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
CC       EXCITABILITY. MAY UNDERLIE A POTASSIUM CURRENT INVOLVED IN
CC       REGULATING THE EXCITABILITY OF SENSORY CELLS OF THE COCHLEA. KCNQ4
CC       CHANNELS ARE BLOCKED BY LINOPIRDIN, XE991 AND BEPRIDIL, WHEREAS
CC       CLOFILIUM IS WITHOUT SIGNIFICANT EFFECT. MUSCARINIC AGONIST
CC       OXOTREMORINE-M STRONGLY SUPPRESS KCNQ4 CURRENT IN CHO CELLS IN
CC       WHICH CLONED KCNQ4 CHANNELS WERE COEXPRESSED WITH M1 MUSCARINNIC
CC       RECEPTORS.
CC   -!- SUBUNIT: MAY FORM HETEROMULTIMERS WITH KCNQ3.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SITUATED AT THE
CC       BASAL MEMBRANE OF COCHLEAR OUTER HAIR CELLS (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
CC       ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN THE OUTER, BUT NOT THE INNER,
CC       SENSORY HAIR CELLS OF THE COCHLEA. SLIGHTLY EXPRESSED IN HEART,
CC       BRAIN AND SKELETAL MUSCLE.
CC   -!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC       CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC       EVERY THIRD POSITION (BY SIMILARITY).
CC   -!- DISEASE: DEFECTS IN KCNQ4 ARE A CAUSE OF NONSYNDROMIC
CC       SENSORINEURAL DEAFNESS TYPE 2 (DFNA2), AN AUTOSOMAL DOMINANT FORM
CC       OF PROGRESSIVE HEARING LOSS.
CC   -!- MISCELLANEOUS: MUTAGENESIS EXPERIMENTS WERE CARRIED OUT BY
CC       EXPRESSING IN XENOPUS OOCYTES KCNQ4 MUTANTS EITHER INDIVIDUALLY
CC       (HOMOMULTIMERS) OR IN COMBINATION WITH WILD-TYPE KCNQ4 (MUT/WT
CC       HOMOMULTIMERS) IN A RATIO OF 1:1, TO MIMIC THE SITUATION IN A
CC       HETEROZYGOUS DFNA2 PATIENT.
CC   -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
CC       SUBFAMILY.
CC   -!- DATABASE: NAME=Hereditary hearing loss homepage;
CC       NOTE=Gene page;
CC       WWW="http://www.uia.ac.be/dnalab/hhh/hhhgenes.html".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF105202; AAD14680.1; -.
DR   EMBL; AF105216; AAD14681.1; -.
DR   EMBL; AF105203; AAD14681.1; JOINED.
DR   EMBL; AF105204; AAD14681.1; JOINED.
DR   EMBL; AF105205; AAD14681.1; JOINED.
DR   EMBL; AF105206; AAD14681.1; JOINED.
DR   EMBL; AF105207; AAD14681.1; JOINED.
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DR   EMBL; AF105208; AAD14681.1; JOINED.
DR   EMBL; AF105209; AAD14681.1; JOINED.
DR   EMBL; AF105210; AAD14681.1; JOINED.
DR   EMBL; AF105211; AAD14681.1; JOINED.
DR   EMBL; AF105212; AAD14681.1; JOINED.
DR   EMBL; AF105213; AAD14681.1; JOINED.
DR   EMBL; AF105214; AAD14681.1; JOINED.
DR   EMBL; AF105215; AAD14681.1; JOINED.
DR   HSSP; Q54397; 1BL8.
DR   Genew; HGNC:6298; KCNQ4.
DR   MIM; 603537; -.
DR   MIM; 600101; -.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003946; KCNQ1_channel.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR000636; M+channel_nlg.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF03520; KCNQ1_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Multigene family; Disease mutation; Deafness; Alternative splicing.
FT   TRANSMEM     98    118       SEGMENT S1 (POTENTIAL).
FT   TRANSMEM    132    152       SEGMENT S2 (POTENTIAL).
FT   TRANSMEM    173    193       SEGMENT S3 (POTENTIAL).
FT   TRANSMEM    202    224       SEGMENT S4 (POTENTIAL).
FT   TRANSMEM    238    258       SEGMENT S5 (POTENTIAL).
FT   DOMAIN      271    292       SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT   TRANSMEM    297    317       SEGMENT S6 (POTENTIAL).
FT   VARSPLIC    378    431       MISSING (IN ISOFORM 2).
FT   VARIANT     274    274       L -> H (IN DFNA2).
FT                                /FTId=VAR_010936.
FT   VARIANT     276    276       W -> S (IN DFNA2).
FT                                /FTId=VAR_008726.
FT   VARIANT     281    281       L -> S (IN DFNA2).
FT                                /FTId=VAR_010937.
FT   VARIANT     285    285       G -> C (IN DFNA2; LOSS OF POTASSIUM
FT                                SELECTIVITY OF THE PORE).
FT                                /FTId=VAR_008727.
FT   VARIANT     285    285       G -> S (IN DFNA2).
FT                                /FTId=VAR_001547.
FT   VARIANT     321    321       G -> S (IN DFNA2).
FT                                /FTId=VAR_008728.
FT   MUTAGEN     285    285       G->S: NO CURRENT (HOMOMULTIMERS); 90% WT
FT                                CURRENT REDUCTION (MU/WT HOMOMULTIMERS).
SQ   SEQUENCE   695 AA;  77091 MW;  A58737BD845E1A3A CRC64;

  Query Match             43.4%;  Score 1989.5;  DB 1;  Length 695;
  Best Local Similarity   60.5%;  Pred. No. 2.3e-106;
  Matches  412;  Conservative   76;  Mismatches  104;  Indels   89;  Gaps   13;

Qy      35 GGGGGLRESRRGKQGARMSLLGKPL--------------SYTSSQSCRRNVKYRRVQNYL 80
           ||||  |          |: ||| ||               |    :|    : :|||:||::
Db      37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy      81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
           ||||||||||||:|| |:||||| ||:||| ||| || :||: ||||||||||||||||:
Db      88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy     141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
           |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db     148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy     201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
           |||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db     208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy     261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
           |:|||:|||||||||||||||| |||||:|:||||||||||||||||||||||||||
Db     268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy     321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
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          |||||||||||| |||||||  || |: |  ::   |||
Db    328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy    359 ----------------------KPHLKALHTCSPTKKEQGEASSSQKLSFKERVRMAS 394
                                 | :   |    |    ||:|   ::  |:|:|| |
Db    388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESS---RMGIKDRIRMGS 444

Qy    395 PRGQSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKP 451
           : ::  |:|  |      |||::   |  |||||||||||||||||| ||||     ||
Db    445 SQRRTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KP 499

Qy    452 VIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDV 511
             |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||
Db    500 RTSAEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDV 558

Qy    512 KDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSML 568
          |||||||||||||| ||||||||||||:|:|    |:|:||   | :: |  |::||:
Db    559 KDVIEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMM 616

Qy    569 GRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDS 628
          |||||||||||||| ||| ||  | : || |::: :| : |:| |: : |||| ||||
Db    617 GRVVKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDH 674

Qy    629 KDLSGSAQNSGCLSRSTSANI 649
          :|:| |||    :||| | |:
Db    675 EDISVSAQTLS-ISRSVSTNM 694
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1831	39.9	842	11	Q923N2	Q923n2 mus musculu
2	1815.5	39.6	723	11	Q923N4	Q923n4 mus musculu
3	1810	39.5	870	11	Q8R498	Q8r498 mus musculu
4	1792	39.1	840	11	Q923N1	Q923n1 mus musculu
5	1787.5	39.0	759	11	Q923N5	Q923n5 mus musculu
6	1755.5	38.3	747	11	Q923N6	Q923n6 mus musculu
7	1634.5	35.6	623	11	Q923N0	Q923n0 mus musculu
8	1633.5	35.6	570	11	Q923N3	Q923n3 mus musculu
9	1230.5	26.8	473	11	Q923M9	Q923m9 mus musculu
10	1220.5	26.6	692	5	Q967F8	Q967f8 caenorhabdi
11	1197	26.1	347	11	Q923M7	Q923m7